SEQUENCE LISTING

<110> CLAYMAN, GARY
NAKASHIMA, TORAHIKO
SPRING, PAUL

<120> METHODS AND COMPOSITIONS OF A NOVEL SERINE PROTEASE INHIBITOR

<130> UTSC:631US

<140> UNKNOWN
<141> 2000-08-31

<150> 60/151,776
<151> 1999-08-31

<160> 21

<170> PatentIn Ver. 2.0

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<210> 2
<211> 391
<212> PRT
<213> Human

<400> 2

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            20                  25                  30

Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
        35                  40                  45

Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
    50                  55                  60

Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Ile Glu Asn Thr Glu
65                  70                  75                  80

Ala Val His Gln Gln Phe Gln Lys Phe Leu Thr Glu Ile Ser Lys Leu
                85                  90                  95

Thr Asn Asp Tyr Glu Leu Asn Ile Thr Asn Arg Leu Phe Gly Glu Lys
            100                 105                 110

Thr Tyr Leu Phe Leu Gln Lys Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr
        115                 120                 125

His Ala Ser Leu Glu Pro Val Asp Phe Val Asn Ala Ala Asp Glu Ser
    130                 135                 140

Arg Lys Lys Ile Asn Ser Trp Val Glu Ser Lys Thr Asn Glu Lys Ile
145                 150                 155                 160

Lys Asp Leu Phe Pro Asp Gly Ser Ile Ser Ser Ser Thr Lys Leu Val
                165                 170                 175

Leu Val Asn Met Val Tyr Phe Lys Gly Gln Trp Asp Arg Glu Phe Lys
            180                 185                 190

Lys Glu Asn Thr Lys Glu Glu Lys Phe Trp Met Asn Lys Ser Thr Ser
        195                 200                 205

Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
    210                 215                 220

Leu Glu Asp Leu Gln Ala Lys Ile Leu Gly Ile Pro Tyr Lys Asn Asn
225                 230                 235                 240

Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
                245                 250                 255

Lys Ile Ile Asp Lys Ile Ser Pro Glu Lys Leu Val Glu Trp Thr Ser
            260                 265                 270

Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
        275                 280                 285

Glu Val Glu Asp Ser Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
    290                 295                 300
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Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
305                 310                 315                 320

Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
                325                 330                 335

Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Ile Gly
            340                 345                 350

Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
        355                 360                 365

Pro Phe Leu Phe Phe Ile Arg His Asn Glu Ser Asn Ser Ile Leu Phe
    370                 375                 380

Phe Gly Arg Phe Ser Ser Pro
385                 390
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<213> Human

<400> 3

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Thr Ser Ala Leu Gly His
            20
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<213> Human

<400> 4

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  1               5                  10                  15

Ser Ser Pro Thr Ser Thr
            20
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<210> 5
<211> 22
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<213> Human

<400> 5

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Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val Val Glu
  1               5                  10                  15

Leu Ser Ser Pro Ser Thr
            20
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<210> 6
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<212> PRT
<213> Human

<400> 6
Glu Glu Gly Thr Glu Ala Ala Ala Gly Thr Gly Gly Val Met Thr Gly
1 5 10 15

Arg Thr Gly His Gly Gly
20

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<212> PRT
<213> Human

<400> 7
Met Asp Ser Leu Gly Ala Val Ser Thr Arg Leu Gly Phe Asp Leu Phe
1 5 10 15

Lys Glu Leu Lys Lys Thr Asn Asp Gly Asn Ile Phe Phe Ser Pro Val
20 25 30

Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
35 40 45

Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
50 55 60

Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Val Arg Ile Lys Ala
65 70 75 80

Glu Gly Lys Glu Ile Glu Asn Thr Glu Ala Val His Gln Gln Phe Gln
85 90 95

Lys Phe Leu Thr Glu Ile Ser Lys Leu Thr Asn Asp Tyr Glu Leu Asn
100 105 110

Ile Thr Asn Arg Leu Phe Gly Glu Lys Thr Tyr Leu Phe Leu Gln Lys
115 120 125

Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr His Ala Ser Leu Glu Pro Val
130 135 140

Asp Phe Val Asn Ala Ala Asp Glu Ser Arg Lys Lys Ile Asn Ser Trp
145 150 155 160

Val Glu Ser Lys Thr Asn Glu Lys Ile Lys Asp Leu Phe Pro Asp Gly
165 170 175

Ser Ile Ser Ser Ser Thr Lys Leu Val Leu Val Asn Met Val Tyr Phe
180 185 190

Lys Gly Gln Trp Asp Arg Glu Phe Lys Lys Glu Asn Thr Lys Glu Glu

```
        195                 200                 205

Lys Phe Trp Met Asn Lys Ser Thr Ser Lys Ser Val Gln Met Met Thr
    210                 215                 220

Gln Ser His Ser Phe Ser Phe Thr Phe Leu Glu Asp Leu Gln Ala Lys
225                 230                 235                 240

Ile Leu Gly Ile Pro Tyr Lys Asn Asn Asp Leu Ser Met Phe Val Leu
                245                 250                 255

Leu Pro Asn Asp Ile Asp Gly Leu Glu Lys Ile Ile Asp Lys Ile Ser
            260                 265                 270

Pro Glu Lys Leu Val Glu Trp Thr Ser Pro Gly His Met Glu Glu Arg
        275                 280                 285

Lys Val Asn Leu His Leu Pro Arg Phe Glu Val Glu Asp Ser Tyr Asp
    290                 295                 300

Leu Glu Ala Val Leu Ala Ala Met Gly Met Gly Asp Ala Phe Ser Glu
305                 310                 315                 320

His Arg Ala Asp Tyr Ser Gly Met Ser Ser Gly Ser Gly Leu Tyr Ala
                325                 330                 335

Gln Lys Phe Leu His Ser Ser Phe Val Ala Val Thr Glu Glu Gly Thr
            340                 345                 350

Glu Ala Ala Ala Ala Thr Gly Ile Gly Phe Thr Val Thr Ser Ala Leu
        355                 360                 365

Gly His Glu Asn Val His Cys Asn His Pro Phe Leu Phe Phe Ile Arg
    370                 375                 380

His Asn Glu Ser Asn Ser Ile Leu Phe Phe Gly Arg Phe Ser Ser Pro
385                 390                 395                 400
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<211> 55
<212> PRT
<213> Human

<400> 8

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Leu Glu Asp Leu Gln Ala Lys Ile Leu Gly Ile Pro Tyr Lys Asn Asn
  1               5                  10                  15

Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
            20                  25                  30

Lys Val Asn Ala Tyr Thr Ser Leu Phe Phe Leu Ser Phe Pro Lys Ala
        35                  40                  45
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Phe Cys Leu Arg Ala Ser Glu
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<210> 9
<211> 390
<212> PRT
<213> Human

<400> 9
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
100 105 110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145 150 155 160

Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
180 185 190

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
195 200 205

Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
260 265 270

Gln Asn Met Arg Glu Thr Arg Val Asp Leu His Leu Pro Arg Phe Lys
275 280 285

Val Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
290 295 300

Val Asp Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Gly Ser
305 310 315 320

Arg Gly Leu Val Leu Ser Gly Val Leu His Lys Ala Phe Val Glu Val
325 330 335

Thr Glu Glu Gly Ala Glu Ala Ala Ala Ala Thr Ala Val Val Gly Phe
340 345 350

Gly Ser Ser Pro Thr Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
370 375 380

Gly Arg Phe Ser Ser Pro
385 390

<210> 10
<211> 390
<212> PRT
<213> Human

<400> 10
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
100 105 110

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Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
        115                 120                 125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
    130                 135                 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145                 150                 155                 160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
                165                 170                 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
            180                 185                 190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
        195                 200                 205

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
    210                 215                 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225                 230                 235                 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
                245                 250                 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
            260                 265                 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
        275                 280                 285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
    290                 295                 300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
305                 310                 315                 320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
                325                 330                 335

Thr Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val Val
            340                 345                 350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
        355                 360                 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
    370                 375                 380

Gly Arg Phe Ser Ser Pro
385                 390
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<210> 11
<211> 415
<212> PRT
<213> Human

<400> 11
Met Glu Asp Leu Cys Val Ala Asn Thr Leu Phe Ala Leu Asn Leu Phe
1 5 10 15

Lys His Leu Ala Lys Ala Ser Pro Thr Gln Asn Leu Phe Leu Ser Pro
20 25 30

Trp Ser Ile Ser Ser Thr Met Ala Met Val Tyr Met Gly Ser Arg Gly
35 40 45

Ser Thr Glu Asp Gln Met Ala Lys Val Leu Gln Phe Asn Glu Val Gly
50 55 60

Ala Asn Ala Val Thr Pro Met Thr Pro Glu Asn Phe Thr Ser Cys Gly
65 70 75 80

Phe Met Gln Gln Ile Gln Lys Gly Ser Tyr Pro Asp Ala Ile Leu Gln
85 90 95

Ala Gln Ala Ala Asp Lys Ile His Ser Ser Phe Arg Ser Leu Ser Ser
100 105 110

Ala Ile Asn Ala Ser Thr Gly Asp Tyr Leu Leu Glu Ser Val Asn Lys
115 120 125

Leu Phe Gly Glu Lys Ser Ala Ser Phe Arg Glu Glu Tyr Ile Arg Leu
130 135 140

Cys Gln Lys Tyr Tyr Ser Ser Glu Pro Gln Ala Val Asp Phe Leu Glu
145 150 155 160

Cys Ala Glu Glu Ala Arg Lys Lys Ile Asn Ser Trp Val Lys Thr Gln
165 170 175

Thr Lys Gly Lys Ile Pro Asn Leu Leu Pro Glu Gly Ser Val Asp Gly
180 185 190

Asp Thr Arg Met Val Leu Val Asn Ala Val Tyr Phe Lys Gly Lys Trp
195 200 205

Lys Thr Pro Phe Glu Lys Lys Leu Asn Gly Leu Tyr Pro Phe Arg Val
210 215 220

Asn Ser Ala Gln Arg Thr Pro Val Gln Met Met Tyr Leu Arg Glu Lys
225 230 235 240

Leu Asn Ile Gly Tyr Ile Glu Asp Leu Lys Ala Gln Ile Leu Glu Leu
245 250 255

Pro Tyr Ala Gly Asp Val Ser Met Phe Leu Leu Leu Pro Asp Glu Ile
260 265 270

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Ala Asp Val Ser Thr Gly Leu Glu Leu Leu Glu Ser Glu Ile Thr Tyr
        275                 280                 285

Asp Lys Leu Asn Lys Trp Thr Ser Lys Asp Lys Met Ala Glu Asp Glu
    290                 295                 300

Val Glu Val Tyr Ile Pro Gln Phe Lys Leu Glu Glu His Tyr Glu Leu
305                 310                 315                 320

Arg Ser Ile Leu Arg Ser Met Gly Met Glu Asp Ala Phe Asn Lys Gly
                325                 330                 335

Arg Ala Asn Phe Ser Gly Met Ser Glu Arg Asn Asp Leu Phe Leu Ser
            340                 345                 350

Glu Val Phe His Gln Ala Met Val Asp Val Asn Glu Glu Gly Thr Glu
        355                 360                 365

Ala Ala Ala Gly Thr Gly Gly Val Met Thr Gly Arg Thr Gly His Gly
    370                 375                 380

Gly Pro Gln Phe Val Ala Asp His Pro Phe Leu Phe Leu Ile Met His
385                 390                 395                 400

Lys Ile Thr Lys Cys Ile Leu Phe Phe Gly Arg Phe Cys Ser Pro
                405                 410                 415
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<210> 12
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<212> PRT
<213> Human

<400> 12
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Gly Thr Glu Ala Ala Ala Ala Thr
  1               5
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<210> 13
<211> 9
<212> PRT
<213> Human

<400> 13
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Val Arg Ile Lys Ala Glu Gly Lys Glu
  1               5
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<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 14
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<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15
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<210> 16
<211> 405
<212> DNA
<213> Human

<400> 16
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tattctttct ttcatttcct aaggcttttt gtctcagggc ttctgagtag gagctggtgg 180
ccagcagtgt caaatagaaa gtgtttctca ctctccagca gctacagatg gatgtctact 240
ggggagcatt aaatagtatg ggtcaggttt attgagaaca actaatccta gaatgtttgg 300
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agaaatggtt ggtatctatg gacccctttc ctggaaaaaa aaaaa 405

<210> 17
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Peptide

<220>
<221> PEPTIDE
<222> (3)
<223> X = Any

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<210> 18
<211> 700
<212> DNA
<213> Human

<400> 18

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cctgtgggca tcttgactgc aattggcatg gtcctcctgg ggacccgagg agccaccgct 180

ccccagttgg aggaggtgtt tcactctgaa aaagagacga agagctcaag aataaaggct 240
gaagaaaaag aggtgattga gaacacagaa gcagtacatc aacaattcca aaagtttttg 300
actgaaataa gcaaactcac taatgattat gaactgaaca taaccaacag gctgtttgga 360
gaaaaaacat acctcttcct tcaaaaatac ttagattatg ttgaaaaata ttatcatgca 420
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gtacagatga tgacacagag ccattccttt agcttcactt 700

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<211> 224
<212> PRT
<213> Human

<400> 19

Met Asp Ser Leu Gly Ala Val Ser Thr Arg Leu Gly Phe Asp Leu Phe
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Lys Glu Leu Lys Lys Thr Asn Asp Gly Asn Ile Phe Phe Ser Pro Val
20 25 30

Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
35 40 45

Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
50 55 60

Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Ile Glu Asn Thr Glu
65 70 75 80

Ala Val His Gln Gln Phe Gln Lys Phe Leu Thr Glu Ile Ser Lys Leu
85 90 95

Thr Asn Asp Tyr Glu Leu Asn Ile Thr Asn Arg Leu Phe Gly Glu Lys
100 105 110

Thr Tyr Leu Phe Leu Gln Lys Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr
115 120 125

His Ala Ser Leu Glu Pro Val Asp Phe Val Asn Ala Ala Asp Glu Ser
130 135 140

Arg Lys Lys Ile Asn Ser Trp Val Glu Ser Lys Thr Asn Glu Lys Ile
145 150 155 160

Lys Asp Leu Phe Pro Asp Gly Ser Ile Ser Ser Ser Thr Lys Leu Val
165 170 175

Leu Val Asn Met Val Tyr Phe Lys Gly Gln Trp Asp Arg Glu Phe Lys
180 185 190

Lys Glu Asn Thr Lys Glu Glu Lys Phe Trp Met Asn Lys Ser Thr Ser
195 200 205

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Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
    210                 215                 220
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<210> 20
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<212> DNA
<213> Human

<400> 20

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gaggacagtt acgatctaga ggcggtcctg gctgccatgg ggatgggcga tgccttcagt 159
gagcacaaag ccgactactc gggaatgtcg tcaggctccg ggttgtacgc ccagaagttc 219
ctgcacagtt cctttgtggc agtaactgag gaaggcaccg aggctgcagc tgccaccggc 279
ataggcttta ctgtcacatc cgccccaggt catgaaaatg ttcactgcaa tcatcccttc 339
ctgttcttca tcaggcacaa tgaatccaac agcatcctct tcttcggcag attttcttct 399
ccttaagatg atcgttgcca tggcattgct gcttttagca aaaaacaact accagtggta 459
ctcatatgaa tatgaaaat                                               478
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<210> 21
<211> 391
<212> PRT
<213> Human

<400> 21

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Lys Ile Ile Asp Lys Ile Ser Pro Glu Lys Leu Val Glu Trp Thr Ser
            260                 265                 270

Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
        275                 280                 285

Glu Val Glu Asp Ser Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
    290                 295                 300

Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
305                 310                 315                 320

Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
                325                 330                 335

Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Ile Gly
            340                 345                 350

Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
        355                 360                 365

Pro Phe Leu Phe Phe Ile Arg His Asn Glu Ser Asn Ser Ile Leu Phe
    370                 375                 380

Phe Gly Arg Phe Ser Ser Pro
385                 390
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